

0950

#6

OIFE

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/825,147

DATE: 09/10/2001

TIME: 11:21:17

Input Set : A:\LEX-0160-USA SEQLIST.txt

Output Set: N:\CRF3\09102001\I825147.raw

ENTERED

4 <110> APPLICANT: Hu, Yi
 5 Kieke, James Alvin
 6 Turner, C. Alexander Jr.
 7 Nehls, Michael C.
 8 Friedrich, Glenn
 9 Zambrowicz, Brian
 10 Sands, Arthur T.
 12 <120> TITLE OF INVENTION: Novel Human Ion Channel Protein and
 13 Polynucleotides Encoding the Same
 16 <130> FILE REFERENCE: LEX-0160-USA
 C--> 18 <140> CURRENT APPLICATION NUMBER: US/09/825,147 OK
 C--> 18 <141> CURRENT FILING DATE: 2001-04-03
 18 <150> PRIOR APPLICATION NUMBER: US 60/194,255
 19 <151> PRIOR FILING DATE: 2000-04-03
 21 <160> NUMBER OF SEQ ID NOS: 3
 23 <170> SOFTWARE: FastSEQ for Windows Version 4.0
 25 <210> SEQ ID NO: 1
 26 <211> LENGTH: 2772
 27 <212> TYPE: DNA
 28 <213> ORGANISM: homo sapiens
 30 <400> SEQUENCE: 1

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| 32 ggcgcagcgg cggcggcgcc gggcgggggg cgcttgggca gcggcatgaa ggatgtggag | 120 |
| 33 tcgggcccgg gcagggtgct gctgaactcg gcagccgcca ggggcgacgg cctgctactg | 180 |
| 34 ctgggcaccc gcgcggccac gctcgggtggc ggcggcggtg gcctgaggga gagccgcccg | 240 |
| 35 ggcaagcagg gggcccggat gagcctgctg gggaagccgc tctcttacac gactagccag | 300 |
| 36 agctgccggc gcaacgtcaa gtaccggcgg gtgcagaact acctgtacaa cgtgctggag | 360 |
| 37 agaccccgcg gctgggcgtt catctaccac gcttctgtt tctccttgt ctttggttgc | 420 |
| 38 ttgattttgt cagtgttttc taccatccct gagcacacaa aattggcctc aagttgcctc | 480 |
| 39 ttgatccttg agttcgtgat gattgtcgtc ttggttttg agttcatcat tcgaatctgg | 540 |
| 40 tctgcggggt gctgttgctg atatagagga tggcaaggaa gactgaggtt tgctcgaaag | 600 |
| 41 cccttctgtg ttatagatac cattgttctt atcgcttcaa tagcagttgt ttctgcaaaa | 660 |
| 42 actcagggtg atatttttgc cacgtctgca ctcagaagtc tccgtttcct acagatcctc | 720 |
| 43 cgcattggtg gcatggaccg aaggggaggc acttggaat tactgggttc agtggtttat | 780 |
| 44 gctcacagca aggaattaat cacagcttgg tacataggat ttttggttct tattttttcg | 840 |
| 45 tctttccttg tctatctggt ggaaaaggat gccataaag agttttctac atatgcagat | 900 |
| 46 gctctctggt ggggcacaat tacattgaca actattgct atggagacaa aactccccta | 960 |
| 47 acttggtctg gaagattgct ttctgcaggc ttgactcc ttggcatttc tttctttgca | 1020 |
| 48 ctctctgccc gcattcttgg ctccaggttt gcattaaaag tacaagaaca acaccgccag | 1080 |
| 49 aaacactttg agaaaagaag gaaccagct gccaacctca ttcagtgtgt ttggcgtagt | 1140 |
| 50 tacgcagctg atgagaaatc tgtttccatt gcaacctgga agccacactt gaaggccttg | 1200 |
| 51 cacacctgca gccctaccaa tcagaagcta agttttaagg agcgagtgcg catggctagc | 1260 |
| 52 cccagggggc agagtattaa gagccgacaa gcctcagtag gtgacaggag gtccccaagc | 1320 |
| 53 accgacatca cagccgaggg cagtcccacc aaagtgcaga agagctggag cttcaacgac | 1380 |
| 54 cgaacccgct tccggccctc gctgcgcctc aaaagttctc agccaaaacc agtgatagat | 1440 |
| 55 gctgacacag cccttggcac tgatgatgta tatgatgaaa aaggatgcca gtgtgatgta | 1500 |
| 56 tcagtggaaag acctcaccac accacttaaa actgtcattc gagctatcag aattatgaaa | 1560 |

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58 attgaacaat attctgctgg tcatctggac atgttggtga gaattaaaag ccttcaaaca 1680
59 cgtgttgatc aaattcttgg aaaagggcaa atcacatcag ataagaagag ccgagagaaa 1740
60 ataacagcag aacatgagac cacagacgat ctccagtatgc tcggtcgggt ggtcaagggt 1800
61 gaaaaacagg tacagtccat agaatccaag ctggactgcc tactagacat ctatcaacag 1860
62 gtccctcgga aaggctctgc ctccagccctc gctttggctt cattccagat cccacctttt 1920
63 gaatgtgaac agacatctga ctatcaaagc cctgtggata gcaaagatct ttcgggttcc 1980
64 gcacaaaaca gtggctgctt atccagatca actagtgcc aactctcgag aggcctgcag 2040
65 ttcatcttga cgccaaatga gttcagtgcc cagactttct acgcgcttag ccctactatg 2100
66 cacagtcaag caacacaggt gccaatagtg caaagcgatg gctcagcagt ggcagccacc 2160
67 aacaccattg caaaccaaat aaatacggca cccaagccag cagccccaac aactttacag 2220
68 atcccacctc ctctcccagc catcaagcat ctgcccaggc cagaaactct gcaccctaac 2280
69 cctgcaggct tacaggaaa gatttctgac gtccaccact gccttgttgc ctccaaggaa 2340
70 atgtgttcagg ttgcacagtc aaatctcacc aaggaccgtt ctatgaggaa aagctttgac 2400
71 atgggaggag aaactctgtt gtctgtctgt cccatgggtg cgaaggactt gggcaaatct 2460
72 ttgtctgtgc aaaactgat caggctcgacc gaggaactga atatacaact ttcaggagg 2520
73 gagtcaagtg gctccagagg cagccaagat ttttacccca aatggaggga atccaaattg 2580
74 ttataactg atgaagaggt ggggtcccga gagacagaga cagacacttt tgatgccgca 2640
75 ccgcagcctg ccagggaagc tgcccttgca tcagactctc taaggactgg aaggtcacga 2700
76 tcatctcaga gcatttgtaa ggcaggagaa agtacagatg ccctcagctt gcctcatgtc 2760
77 aaactgaaat aa 2772

79 <210> SEQ ID NO: 2
80 <211> LENGTH: 923
81 <212> TYPE: PRT
82 <213> ORGANISM: homo sapiens
84 <400> SEQUENCE: 2
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87 Trp Val Lys Ser Gly Ala Ala Ala Ala Ala Ala Gly Gly Gly Arg Leu
88 20 25 30
89 Gly Ser Gly Met Lys Asp Val Glu Ser Gly Arg Gly Arg Val Leu Leu
90 35 40 45
91 Asn Ser Ala Ala Ala Arg Gly Asp Gly Leu Leu Leu Leu Gly Thr Arg
92 50 55 60
93 Ala Ala Thr Leu Gly Gly Gly Gly Gly Gly Leu Arg Glu Ser Arg Arg
94 65 70 75 80
95 Gly Lys Gln Gly Ala Arg Met Ser Leu Leu Gly Lys Pro Leu Ser Tyr
96 85 90 95
97 Thr Ser Ser Gln Ser Cys Arg Arg Asn Val Lys Tyr Arg Arg Val Gln
98 100 105 110
99 Asn Tyr Leu Tyr Asn Val Leu Glu Arg Pro Arg Gly Trp Ala Phe Ile
100 115 120 125
101 Tyr His Ala Phe Val Phe Leu Leu Val Phe Gly Cys Leu Ile Leu Ser
102 130 135 140
103 Val Phe Ser Thr Ile Pro Glu His Thr Lys Leu Ala Ser Ser Cys Leu
104 145 150 155 160
105 Leu Ile Leu Glu Phe Val Met Ile Val Val Phe Gly Leu Glu Phe Ile
106 165 170 175
107 Ile Arg Ile Trp Ser Ala Gly Cys Cys Cys Arg Tyr Arg Gly Trp Gln

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108          180          185          190
109 Gly Arg Leu Arg Phe Ala Arg Lys Pro Phe Cys Val Ile Asp Thr Ile
110          195          200          205
111 Val Leu Ile Ala Ser Ile Ala Val Val Ser Ala Lys Thr Gln Gly Asn
112          210          215          220
113 Ile Phe Ala Thr Ser Ala Leu Arg Ser Leu Arg Phe Leu Gln Ile Leu
114 225          230          235          240
115 Arg Met Val Arg Met Asp Arg Arg Gly Gly Thr Trp Lys Leu Leu Gly
116          245          250          255
117 Ser Val Val Tyr Ala His Ser Lys Glu Leu Ile Thr Ala Trp Tyr Ile
118          260          265          270
119 Gly Phe Leu Val Leu Ile Phe Ser Ser Phe Leu Val Tyr Leu Val Glu
120          275          280          285
121 Lys Asp Ala Asn Lys Glu Phe Ser Thr Tyr Ala Asp Ala Leu Trp Trp
122          290          295          300
123 Gly Thr Ile Thr Leu Thr Thr Ile Gly Tyr Gly Asp Lys Thr Pro Leu
124 305          310          315          320
125 Thr Trp Leu Gly Arg Leu Leu Ser Ala Gly Phe Ala Leu Leu Gly Ile
126          325          330          335
127 Ser Phe Phe Ala Leu Pro Ala Gly Ile Leu Gly Ser Gly Phe Ala Leu
128          340          345          350
129 Lys Val Gln Glu Gln His Arg Gln Lys His Phe Glu Lys Arg Arg Asn
130          355          360          365
131 Pro Ala Ala Asn Leu Ile Gln Cys Val Trp Arg Ser Tyr Ala Ala Asp
132          370          375          380
133 Glu Lys Ser Val Ser Ile Ala Thr Trp Lys Pro His Leu Lys Ala Leu
134 385          390          395          400
135 His Thr Cys Ser Pro Thr Asn Gln Lys Leu Ser Phe Lys Glu Arg Val
136          405          410          415
137 Arg Met Ala Ser Pro Arg Gly Gln Ser Ile Lys Ser Arg Gln Ala Ser
138          420          425          430
139 Val Gly Asp Arg Arg Ser Pro Ser Thr Asp Ile Thr Ala Glu Gly Ser
140          435          440          445
141 Pro Thr Lys Val Gln Lys Ser Trp Ser Phe Asn Asp Arg Thr Arg Phe
142          450          455          460
143 Arg Pro Ser Leu Arg Leu Lys Ser Ser Gln Pro Lys Pro Val Ile Asp
144 465          470          475          480
145 Ala Asp Thr Ala Leu Gly Thr Asp Asp Val Tyr Asp Glu Lys Gly Cys
146          485          490          495
147 Gln Cys Asp Val Ser Val Glu Asp Leu Thr Pro Pro Leu Lys Thr Val
148          500          505          510
149 Ile Arg Ala Ile Arg Ile Met Lys Phe His Val Ala Lys Arg Lys Phe
150          515          520          525
151 Lys Glu Thr Leu Arg Pro Tyr Asp Val Lys Asp Val Ile Glu Gln Tyr
152          530          535          540
153 Ser Ala Gly His Leu Asp Met Leu Cys Arg Ile Lys Ser Leu Gln Thr
154 545          550          555          560
155 Arg Val Asp Gln Ile Leu Gly Lys Gly Gln Ile Thr Ser Asp Lys Lys
156          565          570          575

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157 Ser Arg Glu Lys Ile Thr Ala Glu His Glu Thr Thr Asp Asp Leu Ser
158                               580                               585                               590
159 Met Leu Gly Arg Val Val Lys Val Glu Lys Gln Val Gln Ser Ile Glu
160                               595                               600                               605
161 Ser Lys Leu Asp Cys Leu Leu Asp Ile Tyr Gln Gln Val Leu Arg Lys
162                               610                               615                               620
163 Gly Ser Ala Ser Ala Leu Ala Leu Ala Ser Phe Gln Ile Pro Pro Phe
164 625                               630                               635                               640
165 Glu Cys Glu Gln Thr Ser Asp Tyr Gln Ser Pro Val Asp Ser Lys Asp
166                               645                               650                               655
167 Leu Ser Gly Ser Ala Gln Asn Ser Gly Cys Leu Ser Arg Ser Thr Ser
168                               660                               665                               670
169 Ala Asn Ile Ser Arg Gly Leu Gln Phe Ile Leu Thr Pro Asn Glu Phe
170                               675                               680                               685
171 Ser Ala Gln Thr Phe Tyr Ala Leu Ser Pro Thr Met His Ser Gln Ala
172                               690                               695                               700
173 Thr Gln Val Pro Ile Ser Gln Ser Asp Gly Ser Ala Val Ala Ala Thr
174 705                               710                               715                               720
175 Asn Thr Ile Ala Asn Gln Ile Asn Thr Ala Pro Lys Pro Ala Ala Pro
176                               725                               730                               735
177 Thr Thr Leu Gln Ile Pro Pro Pro Leu Pro Ala Ile Lys His Leu Pro
178                               740                               745                               750
179 Arg Pro Glu Thr Leu His Pro Asn Pro Ala Gly Leu Gln Glu Ser Ile
180                               755                               760                               765
181 Ser Asp Val Thr Thr Cys Leu Val Ala Ser Lys Glu Asn Val Gln Val
182                               770                               775                               780
183 Ala Gln Ser Asn Leu Thr Lys Asp Arg Ser Met Arg Lys Ser Phe Asp
184 785                               790                               795                               800
185 Met Gly Gly Glu Thr Leu Leu Ser Val Cys Pro Met Val Pro Lys Asp
186                               805                               810                               815
187 Leu Gly Lys Ser Leu Ser Val Gln Asn Leu Ile Arg Ser Thr Glu Glu
188                               820                               825                               830
189 Leu Asn Ile Gln Leu Ser Gly Ser Glu Ser Ser Gly Ser Arg Gly Ser
190                               835                               840                               845
191 Gln Asp Phe Tyr Pro Lys Trp Arg Glu Ser Lys Leu Phe Ile Thr Asp
192                               850                               855                               860
193 Glu Glu Val Gly Pro Glu Glu Thr Glu Thr Asp Thr Phe Asp Ala Ala
194 865                               870                               875                               880
195 Pro Gln Pro Ala Arg Glu Ala Ala Phe Ala Ser Asp Ser Leu Arg Thr
196                               885                               890                               895
197 Gly Arg Ser Arg Ser Ser Gln Ser Ile Cys Lys Ala Gly Glu Ser Thr
198                               900                               905                               910
199 Asp Ala Leu Ser Leu Pro His Val Lys Leu Lys
200                               915                               920
202 <210> SEQ ID NO: 3
203 <211> LENGTH: 3111
204 <212> TYPE: DNA
205 <213> ORGANISM: homo sapiens
207 <400> SEQUENCE: 3

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Input Set : A:\LEX-0160-USA SEQLIST.txt
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| | | | | | | | |
|-----|-------------|-------------|------------|-------------|-------------|-------------|------|
| 208 | actcactata | gggctcgagc | ggccgcccgg | gcaggtctcg | cggtgcccgt | ggtgatgcc | 60 |
| 209 | tgccccgcca | ccacgcggga | ggagaggagg | gcggcgccgc | cgggctctgg | gtgaagagcg | 120 |
| 210 | gcgcagcggc | ggcggcggcg | ggcggggggc | gcttgggcag | cggcatgaag | gatgtggagt | 180 |
| 211 | cgggccgggg | caggggtgctg | ctgaactcgg | cagccgccag | ggcgacggc | ctgctactgc | 240 |
| 212 | tgggcacccg | cgcggccacg | ctcggtggcg | gcggcggttg | cctgagggag | agccgcccgg | 300 |
| 213 | gcaagcaggg | ggcccggatg | agcctgctgg | ggaagccgct | ctcttacacg | agtagccaga | 360 |
| 214 | gctgccggcg | caacgtcaag | taccgcgggg | tgcagaacta | cctgtacaac | gtgctggaga | 420 |
| 215 | gaccccgcg | ctgggcgttc | atctaccacg | ctttcgtttt | tctccttgct | tttggttgct | 480 |
| 216 | tgattttgtc | agtgttttct | accatccctg | agcacacaaa | attggcctca | agttgcctct | 540 |
| 217 | tgatcctgga | gttcgtgatg | attgtcgtct | ttggtttgga | gttcattcatt | cgaatctggt | 600 |
| 218 | ctgcgggttg | ctgttgctga | tatagaggat | ggcaagggaag | actgaggttt | gctcgaaagc | 660 |
| 219 | ccttctgtgt | tatagatacc | attgttctta | tcgcttcaat | agcagttggt | tctgcaaaaa | 720 |
| 220 | ctcagggtaa | tatttttgcc | acgtctgcac | tcagaagtct | ccgtttccta | cagatccctc | 780 |
| 221 | gcatggtgcg | catggaccga | aggggaggca | cttgaaatt | actgggttca | gtggtttatg | 840 |
| 222 | ctcacagcaa | ggaattaatc | acagcttggt | acataggatt | tttggttcct | attttttcgt | 900 |
| 223 | ctttccttgt | ctatctggtg | gaaaaggatg | ccaataaaga | gttttctaca | tatgcagatg | 960 |
| 224 | ctctctggtg | gggcacaatt | acattgacaa | ctattggcta | tggagacaaa | actcccctaa | 1020 |
| 225 | cttggctggg | aagattgctt | tctgcaggct | ttgcactcct | tggcatttct | ttctttgcac | 1080 |
| 226 | ttcctgccgg | cattcttggtc | tcaggttttg | cattaaaagt | acaagaacaa | caccgccaga | 1140 |
| 227 | aacactttga | gaaaagaagg | aacccagctg | ccaacctcat | tcagtgtggt | tggcgtagtt | 1200 |
| 228 | acgcagctga | tgagaaatct | gtttccattg | caacctgga | gccacacttg | aaggccttgc | 1260 |
| 229 | acacctgcag | ccctaccaat | cagaagctaa | gttttaagga | gcgagtgcgc | atggctagcc | 1320 |
| 230 | ccaggggcca | gagtattaag | agccgacaag | cctcagtagg | tgacaggagg | tccccaagca | 1380 |
| 231 | ccgacatcac | agccgagggc | agtcccacca | aagtgcagaa | gagctggagc | ttcaacgacc | 1440 |
| 232 | gaaccgcgtt | cgggccctcg | ctgcgcctca | aaagttctca | gccaaaacca | gtgatagatg | 1500 |
| 233 | ctgacacagc | ccttggcact | gatgatgtat | atgatgaaaa | aggatgccag | tgtgatgtat | 1560 |
| 234 | cagtgggaaga | cctcacccca | ccacttaaaa | ctgtcattcg | agctatcaga | attatgaaat | 1620 |
| 235 | ttcatgttgc | aaaacggaag | tttaaggaaa | cattacgtcc | atatgatgta | aaagatgtca | 1680 |
| 236 | ttgaacaata | ttctgctggt | catctggaca | tgttgtgtag | aattaaaagc | cttcaaacac | 1740 |
| 237 | gtgttgatca | aattcttggg | aaagggcaaa | tcacatcaga | taagaagagc | cgagagaaaa | 1800 |
| 238 | taacagcaga | acatgagacc | acagacgatc | tcagtatgct | cggtcgggtg | gtcaagggtg | 1860 |
| 239 | aaaaacaggt | acagtccata | gaatccaagc | tggactgcct | actagacatc | tatcaacagg | 1920 |
| 240 | tccttcggaa | aggctctgcc | tcagccctcg | ctttggcttc | attccagatc | ccaccttttg | 1980 |
| 241 | aatgtgaaca | gacatctgac | tatcaaagcc | ctgtggatag | caaagatctt | tcgggttccg | 2040 |
| 242 | cacaaaacag | tggtgctta | tccagatcaa | ctagtgccaa | catctcgaga | ggcctgcagt | 2100 |
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| 244 | acagtcaagc | aacacaggtg | ccaattagtc | aaagcgatgg | ctcagcagtg | gcagccacca | 2220 |
| 245 | acaccattgc | aaaccaaata | aatacggcac | ccaagccagc | agccccaaca | actttacaga | 2280 |
| 246 | tcccacctcc | tctcccagcc | atcaagcate | tgcccaggcc | agaaactctg | caccctaacc | 2340 |
| 247 | ctgcaggctt | acaggaaagc | atttotgacg | tcaccacctg | ccttgttgcc | tccaaggaaa | 2400 |
| 248 | atgttcagg | tgacagtcga | aatctcacca | aggaccgttc | tatgaggaaa | agctttgaca | 2460 |
| 249 | tgggaggaga | aactctgttg | totgtctgtc | ccatggtgcc | gaaggacttg | ggcaaattctt | 2520 |
| 250 | tgtctgtgca | aaacctgatc | aggtcgaccg | aggaactgaa | tatacaactt | tcaggggagt | 2580 |
| 251 | agtcaagtgg | ctccagaggg | agccaagatt | tttaccctaa | atggagggaa | tccaaattgt | 2640 |
| 252 | ttataactga | tgaagaggtg | ggtcccgaag | agacagagac | agacactttt | gatgcccgcac | 2700 |
| 253 | cgcagcctgc | caggggaagct | gcctttgcat | cagactctct | aaggactgga | aggtcacgat | 2760 |
| 254 | catctcagag | catttgtaag | gcaggagaaa | gtacagatgc | cctcagcttg | cctcatgtca | 2820 |
| 255 | aactgaaata | agttcttcat | tttctttcca | ggcatagcag | ttcttttagcc | atacatatca | 2880 |
| 256 | ttgcatgaac | tatttcgaaa | gcccttctaa | aaagttgaaa | ttgcaagaat | cgggaagaac | 2940 |

VERIFICATION SUMMARY

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Input Set : A:\LEX-0160-USA SEQLIST.txt
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L:18 M:270 C: Current Application Number differs, Replaced Current Application No
L:18 M:271 C: Current Filing Date differs, Replaced Current Filing Date